SEQUENCE LISTING

<110> NAGY et al.

<120> HUMAN POLYPEPTIDES CAUSING OR LEADING TO THE KILLING
       OF CELLS INCLUDING LYMPHOID TUMOR CELLS

<130> GPCG-P01-003

<140> 10/001934
<141> 2001-11-15

<150> PCT/US01/15625
<151> 2001-05-14

<150> EP 00 11 0065.0
<151> 2000-05-12

<150> US 60/238,762
<151> 2000-10-06

<160> 62

<170> PatentIn version 3.2

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CDR3, MS-GPC8-6-2-VH-CDR3, MS-GPC8-6-13-VH-CDR3, MS-GPC8-6-19-VH-CDR3, MS-GPC8-
6-27-VH-CDR3, MS-GPC8-6-45-VH-CDR3, MS-GPC8-10-57-VH-CDR3, MS-GPC8-27-7-VH-CDR3,
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<223>  "Xaa" represents any amino acid residue

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8

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Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ser His
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Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35              40              45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50              55              60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65              70              75              80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ile Gln Leu
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His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100             105
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Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20              25              30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35              40              45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50              55              60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65              70              75              80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ser Ile
                85              90              95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
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11

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12

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14

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17

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18

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20

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<400>  37
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            20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
            35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
        50   55   60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Gln Tyr Gly His Arg Gly Gly Phe Asp His Trp Gly Gln
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Gly Thr Leu Val Thr Val Ser Ser
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<213>   artificial sequence

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<222>   (1)..(109)

<400>   38

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Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asn Glu
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Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
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22

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<211> 118
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC6-VH
<222> (1)..(118)

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Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
        50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Tyr Gly Arg Tyr Ser Pro Asp Leu Trp Gly Gln Gly Thr
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Leu Val Thr Val Ser Ser
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
            35   40   45

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Leu Pro
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Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
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<213> artificial sequence

<220>
<221> MS-GPC8-VH, MS-GPC8-1-VH,MS-GPC8-6-VH, MS-GPC8-9-VH,MS-GPC8-10-VH,MS-GPC8-17-VH,MS-GPC8-18-VH,MS-GPC8-27-VH,MS-GPC8-6-2-VH,MS-GPC8-6-13-VH,MS-GPC8-6-27-VH,MS-GPC8-6-45-VH,MS-GPC8-6-47-VH,MS-GPC8-10-57-VH,MS-GPC8-27-7-VH, MS-GPC8-27-10-VH, MS-GPC8-27-41-VH
<222> (1)..(120)

<400> 41

```
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
                100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
            115                 120
```

<210> 42
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-VL
<222> (1)..(109)

<400> 42

```
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
                20                  25                  30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Pro Gln
                85                  90                  95

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100                 105
```

<210> 43
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC10-VH
<222> (1)..(120)

<400> 43

```
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
                20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
            35                  40                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
        50                  55                  60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
```

```
Cys Ala Arg Gln Leu His Tyr Arg Gly Gly Phe Asp Leu Trp Gly Gln
            100         .       105             110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  44
<211>  109
<212>  PRT
<213>  artificial sequence

<220>
<221>  MS-GPC10-VL
<222>  (1)..(109)


<400>  44

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50              55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Thr Met
                85                  90                  95

Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100             105

<210>  45
<211>  109
<212>  PRT
<213>  artificial sequence

<220>
<221>  MS-GPC8-6-2-VL
<222>  (1)..(109)

<400>  45

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ser Asn
            20                  25                  30
```

```
Tyr Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35              40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50              55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70              75                      80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                85              90                  95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100             105
```

<210> 46
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-VL
<222> (1)..(109)

<400> 46

```
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35              40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50              55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70              75                      80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                85              90                  95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100             105
```

<210> 47
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-19-VL
<222> (1)..(109)

27

<400> 47

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ser Asn
                20   25   30

Tyr Val Ala Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
            85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210>   48
<211>   109
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-10-VL
<222>   (1)..(109)

<400>   48

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
                20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg
            85   90   95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210>   49

<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-27-VL
<222> (1)..(109)

<400> 49
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Asp Ser Asn Ile Gly Ala Asn
            20   25   30

Tyr Val Thr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210> 50
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-17-VL
<222> (1)..(109)

<400> 50

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ser Val
                    85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100   105

<210> 51
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-45-VL
<222> (1)..(109)

<400> 51
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Pro Asn Ile Gly Ser Asn
                20   25   30

Tyr Val Phe Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
                35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                    85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100   105

<210> 52
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-27-VL
<222> (1)..(109)

<400> 52
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
                20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
                35   40   45

30

```
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
    65                  70                  75

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn
80                  85                  90                  95

Val His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100                 105             109
```

```
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1                   5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ser Asn
                20                  25                  30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                85                  90                  95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100                 105
```

```
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
```

```
            1                     5                          10                           15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn
            20                      25                      30

Tyr Val Thr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                      40                      45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
            50                      55                      60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                      70                      75                      80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                        85                      90                      95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                        100                     105
```

```
<210>  55
<211>  109
<212>  PRT
<213>  artificial sequence

<220>
<221>  MS-GPC8-27-7-VL
<222>  (1)..(108)

<400>  55
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1                   5                       10                      15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
            20                      25                      30

Tyr Val Gly Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                      40                      45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
            50                      55                      60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                      70                      75                      80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val
                        85                      90                      95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                        100                     105
```

```
<210>  56
<211>  109
<212>  PRT
<213>  artificial sequence
```

<220>
<221> MS-GPC8-10-57-VL
<222> (1)..(109)

<400> 56
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
                20   25   30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg
                85   90   95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210> 57
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-27-10-VL
<222> (1)..(108)

<400> 57
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn
                20   25   30

Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val
                85   90   95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly

33

<210> 58
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-27-41-VL
<222> (1)..(108)

<400> 58
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
            20   25   30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val
                85   90   95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210> 59
<211> 8
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC1-VL-CDR3
<222> (1)..(8)

<400> 59

Gln Ser Tyr Asp Phe Asn Glu Ser
1   5

<210> 60
<211> 8
<212> PRT
<213> artificial sequence

<220>

<221> MS-GPC8-6-VL-CDR3,MS-GPC8-6-2-VL-CDR3,MS-GPC8-6-13-VL-CDR3, MS-GPC8-6-19-
VL-CDR3,MS-GPC8-6-27-VL-CDR3,MS-GPC8-6-45-VL-CDR3,MS-GPC8-6-47-VL-CDR3
<222>   (1)..(8)

<400>   60

Gln Ser Tyr Asp Tyr Asp His Tyr
1   5

<210>   61
<211>   10
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC10-VH-CDR3
<222>   (1)..(10)

<400>   61

Gln Leu His Tyr Arg Gly Gly Phe Asp Leu
1   5   10

<210>   62
<211>   12
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC6-VL-CDR1
<222>   (1)..(12)

<400>   62

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1   5   10